

As the Examiner noted, Applicant elected claims 9, 10, and 12-14 and added claims 33-72 in the response submitted 3, January 2001 to the restriction requirement mailed 3 October 2000. Therefore, claim 11 (current claim Group II) is a pending but non-elected claim, and no additional election with respect to claim 11 is needed. Nonetheless, in order to clarify the matter, Applicant now confirms the election submitted in the Response to Restriction Requirement and Preliminary Amendment filed 3 January 2001, electing claims 9, 10, 12-14 and new claims 33-72.

**Applicant's traversal of Examiner's requirement to elect a single nucleic acid sequence**

In connection with the Examiner's requirement that Applicant elect a single nucleic acid sequence, Applicant respectfully submits that this requirement is improper and requests that the Examiner reconsider and withdraw the requirement.

In particular, Applicant requests that the Examiner apply 1192 OG 68 (as presented in MPEP 803.04) as is proper in this case. Applicant observes that the Foreword to the MPEP indicates that "Examiners will be governed by the applicable statutes, rules, decisions, and orders and instructions issued by the Commissioner and the Assistant Commissioners. Orders and Notices still in force which relate to the subject matter included in this Manual are incorporated in the text." (Emphasis added.) Clearly, 1192 OG 68 is such a "Notice still in force", and therefore is a Notice by which the Examiner must be governed. Therefore, the decision to follow or not follow 1192 OG 68 (and MPEP 803.04) is not a matter of discretion for the Examiner, but rather is a requirement.

Looking at the Notice itself, 1192 OG 68 provides that "in most cases, up to ten (10) independent and distinct nucleotide sequences will be examined in a single application without restriction." The text also indicates that "In some exceptional cases, the complex nature of the claimed material, for example a protein amino acid sequence reciting three dimensional folds, may necessitate that the reasonable number of sequences to be selected be less than ten (10)." (Emphasis added.) Notably, it is only for "exceptional" cases that the number may be limited to less than 10.

The specific reference to "exceptional cases" is directly contrary to the Examiner's requirement in the present case. There is nothing "exceptional" about the present

sequences and claims that could justify limiting Applicant to a single sequence, and the Examiner has not even presented anything supporting a conclusion that this application is an "exceptional case." Quite to the contrary, in the telephonic interview with SPE Low on August 22, 2001 concerning the restriction to a single sequence in this case, SPE Low stated that the Art Unit was limiting all applications to a single sequence. Applicant respectfully submits that limiting all applications to a single sequence is directly contrary to both the spirit and the text of 1192 OG 68 and is therefore improper.

The practice stated by SPE Low of limiting all applications to a single sequence effectively indicates that each and every application is an "exceptional case". This cannot be either logically or practically true, and makes a nullity of the entirety of 1192 OG 68. Interpreting an exception to a general rule in such a manner as to make a nullity of the rule is incorrect and improper. Therefore, limiting non-exceptional applications such as the present case to a single sequence represents a violation of a current, valid Notice from the Commissioner.

Therefore, Applicant respectfully requests that the Examiner follow the required restriction practice, and withdraw the present limitation to a single nucleic acid sequence.

**Request for rejoinder of claim 11**

In paragraph 8-9 of the present office action, the Examiner stated that Applicant's comments concerning the absence of additional search burden if claim 11 was rejoined were unpersuasive. Applicant requests that the Examiner reconsider that conclusion.

It is understood by those of ordinary skill in the art, that searches based on nucleic acid and/or polypeptide sequences must be performed with cross-reference between both types of sequences in order to be complete. Indeed, most current sequence search tools are capable of automatically performing such searches, e.g., using a polypeptide sequence as a query sequence to search for both polypeptide sequences and for nucleic acid sequences encoding that polypeptide. Therefore, as Applicant previously pointed out, there would be no additional search burden on the Examiner, and rejoinder of claim 11 with the currently elected claims is proper, and Applicant respectfully requests that rejoinder.